

FIG. 1

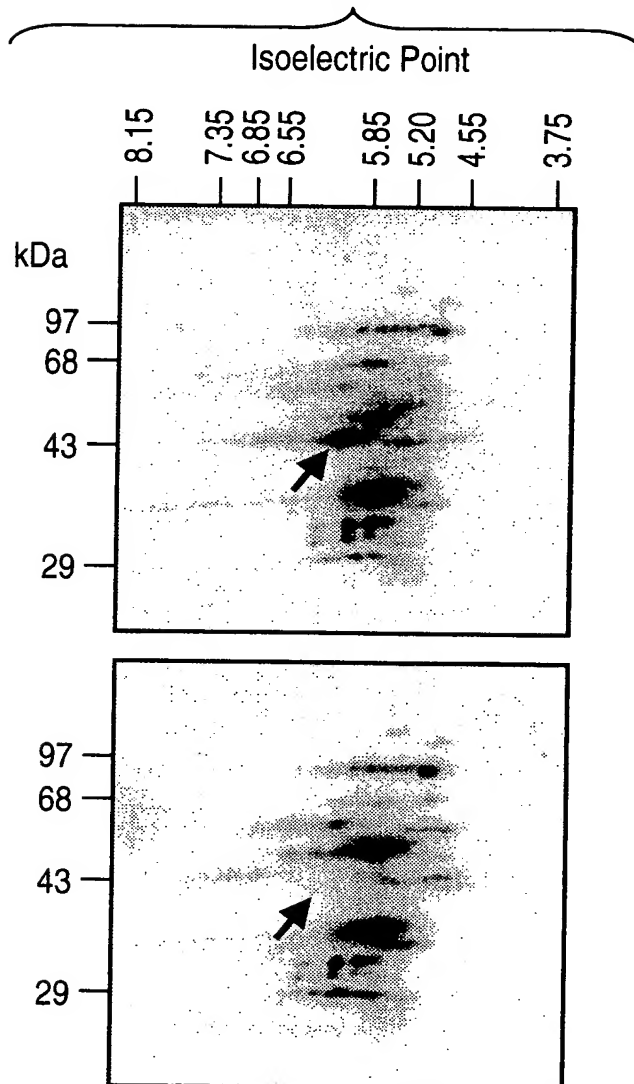


FIG. 2

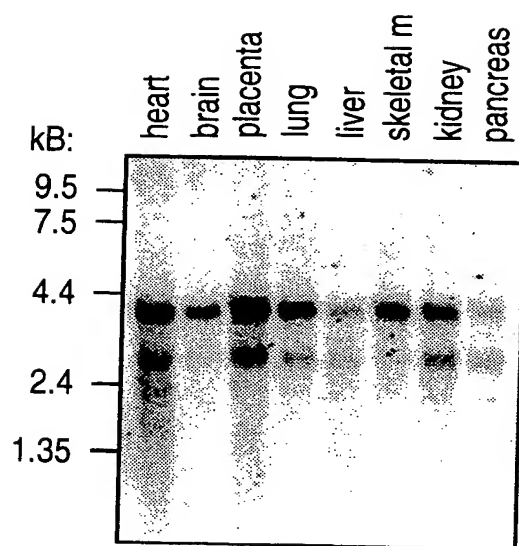


FIG. 3A

1 CGCGGAAGGCGAGAATGGGACTCCAAGCCTGCCTCCTAGGGCTCTTTGGCCCTCATCCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCG  
     M G L Q A C L L G L F A L I L S G K C S Y S P E P D  
 91 ACCAGCGGAGGACGCTGCCCGGAGCTGGGTGTCCCTGGGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTTTGCCCTGAGACAGC  
     Q R R T L P P G W V S L G R A D P E E L S L T F A L R Q Q  
 181 AGAATGTGGAAGACTCTCGGAGCTGGTGCAGGCTGTGTGGATCCAGCTCTCCTCAATACGGAATAACCTGACCCCTAGAGAATGTGG  
     N V E R L S E L V Q A V S D P S S P Q Y G K Y L T L E N V A  
 271 CTGATCTGGTGAGGCCATCCCCACTGACCCCTCCACACGGTGCAAAATGGCTCTTGGCAGCGGAGCCAGAAAGTGCCTATCTCTGTGATCA  
     D L V R P S P L T L H T V Q K W L L A A G A Q K C H S V I T  
 361 CACAGGACTTTCTGACTTGTGGCTGAGCATCCGACAAGCAGAGCTGTCTCCCTGGGGCTGAGTTTCATCATCATATGTGGGAGGACCTA  
     Q D F L T C W L S I R Q A E L L L P G A E F H H Y V G G P T  
 451 CGGAACCCCATGTTGTAAGTCCCCACATCCCTACAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGACTGCACCATTT  
     E T H V V R S P H P Y Q L P Q A L A P H V D F V G G L H H F  
 541 TTCCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGACTGTAGGCCCTGCATCTGGGGGTAACCCCTCTGTGATCC  
     P P T S S L R Q R P E P Q V T G T V G L H L G V T P S V I R  
 631 GTAAGCGATACAACTTGACCTCACAAGACGTTGGGCTCTGGCACCAAGCAATAACAGCCAGCCTGTGCCAGTTCTCTGGAGCAGTATTTC  
     K R Y N L T S Q D V G S G T S N N S Q A C A Q F L E Q Y F H  
 721 ATGACTCAGACCTGGCTCAGTTCAATCGGCTCTTGGTGGCAACTTTGCACATCAGGCATCAGTAGCCCGTGTGGTGGACAACAGGGCC  
     D S D L A Q F M R L F G G N F A H Q A S V A R V V G Q Q G R  
 811 GGGCCGGCGGATTGAGGCCAGTCTAGATGTGCAGTACCTGATGAGTGTGTGGTGGCAACATCTCCACCTGGGTCTACAGTAGCCCTG  
     G R A G I E A S L D V Q Y L M S A G A N I S T W V Y S S P G  
 901 GCCGGCATGAGGACAGGAGCCCTTCTGTCAGTGGCTCATGTCTCAGTAATGAGTCAGCCCTGCCACATGTGCATACTGTGAGCTATG  
     R H E G Q E P F L Q W L M L L S N E S A L P H V H T V S Y G

FIG. 3B

991 GAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCAACACTGAGCTCATGAAGGCTGCTGGGCTCACCCTGCTCT  
     D D E D S L S S A Y I Q R V N T E L M K A A A R G L T L L F  
 1081 TCGCCTCAGGTGACAGTGGGGCCGGTGTGGTCTGTCTCTGGAAGACACCAAGTTCGGCCCTACCTTCCCTGCCCTCCAGCCCCCTATGTCA  
     A S G D S G A G C W S V S G R H Q F R P T F P A S S P Y V T  
 1171 CCACAGTGGAGGCACATCCTTCCAGGAACCTTTCCTCATCACAAATGAATTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGT  
     T V G G T S F Q E P F L I T N E I V D Y I S G G F S N V F  
 1261 TCCCACGGCCTTCATACCAGGAGGAAGCTGTAAAGAGTTCCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGCCAGTG  
     P R P S Y Q E E A V T K F L S S S P H L P P S S Y F N A S G  
 1351 GCCGTGCCCTACCCAGATGTGGCTGCACTTTCTGATGGCTACTGGTGGTCAGCAACAGAGTGCCCATTCATGGGTGTCGGGAACCTCGG  
     R A Y P D V A A L S D G Y W V V S N R V P I P W V S G T S A  
 1441 CCTCTACTCCAGTGTGGGGGATCCTATCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCTCTTGGCTTTCTCAACCCAA  
     S T P V F G G I L S L I N E H R I L S G R P P L G F L N P R  
 1531 GGCTCTACCAGCAGCATGGGCAGGACTCTTTGATGTAAACCCGTGGCTGCCATGAGTCCTGTCTGGATGAAGAGGTAGAGGGCCAGGGTT  
     L Y Q Q H G A G L F D V T R G C H E S C L D E E V E G Q G F  
 1621 TCTGCTCTGGTCCCTGGGATCCTGTAAACAGGCTGGGGAACACCCAACTTCCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCCT  
     C S G P G W D P V T G W G T P N F P A L L K T L L N P \*  
 1711 TTCCATACAGGAGATGGCTTGTCCTGCCCTGAAGCTGGCAGTTCAGTCCCTTATTCTGCCCTGTGGAAAGCCCTGCTGAACCCCTCA  
 1801 ACTATTGACTGCTGACACAGCTTATCTCCCTAAACCCTGAAATGCTGTGAGCTTGACTCCCAACCCCTACCATGCTCCATCATACT  
 1891 CAGGTCTCCCTACTCCTGCTTAGATTCCCTCAATAAGATGCTGAACCTAGCATTTTGTGAATGCTCTCCCTCCGCATCTCATCTTCTC  
 1981 TTTTCAATCAGGCTTTTCCAAAGGTTGTATACAGACTCTGTGCACATATTCACTTGATATTCAATCCCCAATTCACTGCAAGGAGACCT  
 2071 CTACTGTCAACCGTTTACTCTTTCCTACCCCTGACATCCAGAAACAATGGCCCTCCAGTGCATACCTTCTCAATCTTTGCTTTATGGCCTTTCC  
 2161 ATCATAGTTGCCCACTCCCTCTCCTTACTTAGCTTCCAGGCTTAACTTCTCTGACTACTCTTGTCTCTCTCTCATCAATTTCTGCTT  
 2251 CTTTCATGGAATGCTGACCTTCAATTGCTCCATTGCTCTTCTCAGTTTACTCATTTGTCCTCCCTGGAACAATCACTGACATC  
 2341 TACAACCATTACCATCTCAATAATAAGACTTTCTATCCAAATAATGATTGATACCTCAAA

## FIG. 3C

2401 TGTAAGATGCGTGATACACAATTTTCATCGTCCACCTTCCCAACCCCAACAATTCCATCTCGTTTCTTCTGGTAAATGATGCTATGC  
 /AAAAAAAAAAAA...  
 2491 TTTTCCAAACCAAGCCAGAAACCTGTGTCAATCTTTTCACCCCAACCTTCAATCAACAAGTCCTCAATCAACAAGTCCTACTGACTGCACAT  
 2581 CTTAAATATATCTTTATCAGTCCACAAAGTCCCTCCCAATTATATTTCCCAAGTATATCTAGAACTTATCCACTTATATATCCCACTGCTACT  
 2671 ACCTTAGTTAGGGCTATATCTCTTGAAAAAAGTGTCCTTACTTCCGCAATCCCAAGTCAATCTTCCAGAGTAAATGCAAAATCCC  
 2761 ATCAGGCCACTTGGATGAAAACCCCTTCAAGGATTACTGGATAGAAATTCAGGCTTTCCCTCCASCCCCAATCATAGCTCACAACCTTC  
 2851 CTTGCTATTTGTTCTTAAGTAAAAAATCAATTTTCCCTCCTCCCTCCCAACCCCAAGGAACTCTCACTCTTGCTCAAGCTGTCCGTC  
 2941 CCTTACCACCCCTGATACAACTGCCAGGTTAAATTTCCAGAAATTTCTGCAAGACTCAGTTCAGAAAGTCACCTTCTTTCGTGAATGTTTGA  
 3031 TTCCCTGAGGCTACTTTTATTTTGGTATGGCTGAAAAATCCTAGATTTTCTAAACAAAACCTGTTTGAATCTTGGTCTTGATATGGACTAG  
 3121 GAGAGAGACTGGGTCAAGTAAGCTTATCTCCCTGAGGCTGTTTCCCTCGTCTGTTAAGTGTGAATATCAATACCTGCCCTTTCATATACACC  
 3211 AGGGAATAAAGTGGAATAATGTTGATAAACAGTGTGGCACCCTGGAAGTAGGTGGCAGATGTTAAACGCCCTTCCCTCCCTTGCACATGGCC  
 3301 CCCGTGCTACCTCTAGCATTTGTAACGACCACATAGTATTGAAATGGCCAGTTTACTTGTCTGCTTCCCTTCCCAAGACCGTTGGTGCC  
 3391 TAGAGGACTAGAAATCGTGTCCCTATTTAACTTTGTGTTCCAGGTCCTAGCTCAGGAGTTGGCAAAATTAAGAATTAAATGTCTGTCTACACCG  
 3481 AAACAA

FIG. 4A

CLN2	1	.....MCLQACILGLFALILSGKCSYSPEFDQR.....RTLPPGMV.....
PsCP	1	MKSSAAKQTVLCLNRYAV.VALPLALASFAAFGASP.....ASTLWAPTDTKAEVTPAQVEAR.S
XaCP	1	.....MKIEKTAITVAIALAMSSLSAHAEADAVSTHTQAA MSPASTQVLAASSTSAATTGNATTLNMTGSPRTD
CLN2	37	..SLGRADPEELSLTFALRQONVERLSELVQAVSDPSSPQYCKYLTLENVADLVRPSPSLTLHTVQKWLILAGAKCHSV
PsCP	59	AAPLLELAAGETAHIVSLKLRDEAQLKOLAQAVNQPGNAQFGKFLKRRQFLSQFAPTEAQVQAVVAHLKNGFVNIH.V
XaCP	71	GAAVTALADHPLEHVEVALKLRNPDALQTFLAGVITPGSALFGKFLTPSQETERFEGPTQSQVDAVVAHLQCAAGFTNIE.V
CLN2	115	ITQDFITCWL SIQAEILLPGAEEHHVGGPTETHVVRSPHPYQLPQALAPHVDVGGIHHFPPTSSIR...QRPEQVIT
PsCP	138	VPNRLLISADGSAGAVKAAENTPLVRYQLNGKAGYA..NTAPAQVPPQLGEIVGSLGLQNVTRAHPMLKVGERSAAK..
XaCP	150	APNRLLISADGTAGAAATNGERTSIKRESANGREFFA..NDAPALVPASLGD SVN AVLGLQNVSVKHTITHHVHPEDVTVP
CLN2	192	GTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFGGNFAHQASVARVVGOQGRGRAGI
PsCP	214	....TLAAGTAKGHNTEFFTIIYDASSAPTAAHTTVGIIITIGVSDTLQDLQOFTSA..NGLASVNTQITIGSSNGDY
XaCP	228	GPVNGTQAAA AVAAAHHPQDFAAIYGGSSLPAAHTNTAVGIIITWGSITQTVTDLNSFTSG..AGLAEVNSTITKVGS..GTF
CLN2	272	.....EASLDVQYLM.SAGANISTWV.YSSIPGRHEGQEPFLQWMLISNESALPH...VHTVSMGDE.DSLSSAY
PsCP	287	SDPQQGGQGEWDLDSQSIIVGSAGCAVQQLIFYMADQSASGNTGLTQA....FNQAVSDNVAKVINVSLGNCERADANADGT
XaCP	304	ANDPDSNGEWSLDSQDIVGTAGG.VKQLIFYTSANGDSSSSGTTDAGITASYNRAVTDNTAKLINVSLGEDETAAQOSGT
CLN2	337	IQRVNTELMKAAARGCLTLLFASGDSGA.....GCWSVSGR.....HQFRPTFPASSPYVTIVGGTSFOEPFL
PsCP	362	LOAEDRIFATAAQQTFSVSSGDEGYE.....CNRGYPDGSI.....YSVSWPASSPNVIAVGGTTLTYS
XaCP	383	QAADDAIFQAAVAAQQTFSIASGDAGVYQWSTDPTSGSPGYVANSAGTVKIDLTHTYSVSEPASSPYIVQVGGTTL.STSG

# FIG. 4B

CLN2	399	I	N	E	I	V	D	I	S	G	G	F	S	N	V	F	R	P	S	.....	Y	Q	E	E	A	V	T	K	F	L	S	S	P	H	L	P	P	S	S	Y	F	N	A	S	C	R	A	Y	P	D	V	...	A	A	L	S	D	G	Y	W	V	S	N	R	V	P	I	P								
?SCP	427	G	A	Y	S	.	N	E	T	V	N	E	G	L	.....	D	S	N	G	K	L	W	A	T	G	G	G	Y	S	V	T	E	S	K	P	S	W	Q	S	M	V	S	G	T	P	G	R	R	L	L	P	D	I	S	F	D	A	A	Q	G	T	G	A	L	I	N	Y	.	G	Q	L	Q				
XaCP	462	T	T	W	S	.	G	E	T	V	N	E	G	L	S	A	I	A	P	S	Q	G	D	N	N	Q	R	L	W	A	T	G	G	V	S	L	Y	E	A	P	S	W	Q	S	S	V	S	.	S	T	K	R	V	G	P	D	L	A	F	D	A	A	S	S	S	G	A	L	I	V	N	.	G	S	T	E

CLN2	470	W	S	G	T	S	A	S	T	P	M	F	G	G	L	S	L	N	E	H	R	I	L	S	G	R	P	P	L	G	F	L	N	P	R	L	Y	Q	H	G	A	G	...	L	F	D	V	T	R	G	C	H	E	S	C	L	D	E	E	V	E	G	Q	G	F	C	S	G	P	G	W	D	P	V	T
?SCP	497	Q	I	G	G	T	S	L	A	S	P	I	F	V	G	L	W	A	R	L	Q	S	...	A	N	S	N	S	L	G	F	P	A	A	S	F	Y	S	A	I	S	S	T	P	S	L	V	H	D	V	K	S	G	.....	N	N	G	Y	G	G	Y	G	N	A	G	T	G	W	D	Y	P	T			
XaCP	539	Q	V	G	G	T	S	L	A	S	P	I	F	V	G	A	F	A	R	I	E	S	...	A	A	N	N	A	I	G	F	P	A	S	K	F	Y	Q	A	F	P	T	Q	T	S	L	L	H	D	V	T	S	G	.....	N	N	G	Y	Q	S	H	G	Y	T	A	T	G	F	D	E	A	T			

CLN2	547	G	W	G	T	P	N	F	P	A	L	K	T	L	L	N	P	.....									
PSCP	567	G	W	G	S	L	D	I	.	A	K	I	S	A	V	I	R	S	N	G	F	G	H	.....			
XaCP	609	G	F	G	S	F	D	I	.	G	K	I	N	T	Y	A	Q	A	N	W	T	G	G	G	G	S	T

FIG. 5A

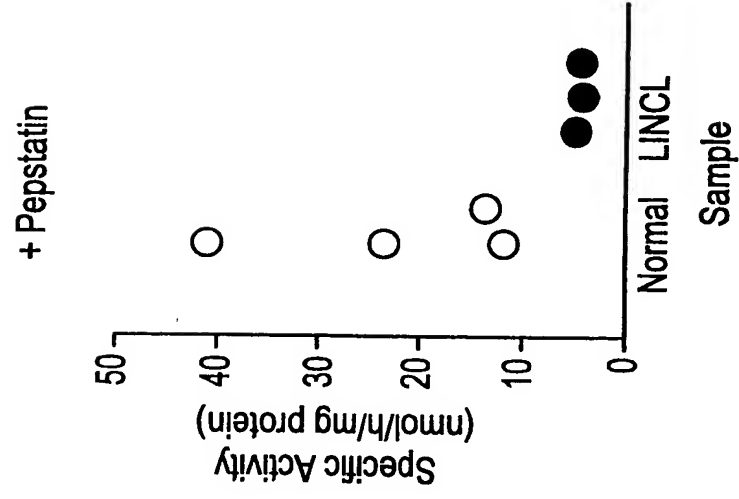


FIG. 5B

